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R70141	y148g11.s1
A1918219	tn08f10.x
B110202	UI-R-CA0-
BF401780	UI-R-CA0-
B1403166	MI-P-CPI-
B114223	UI-R-CA0-
BF416269	UI-R-CA0-
B1119093	AR023A09P
BF404955	UI-R-CAI-
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BM195829	C0317E11-
A1741034	w225f08.x
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BM193296	TCCBAP1E89
BM146800	TCCAP1E73
BB096875	BB096875
BG243742	6023357051
BH305262	CH230-4B1
AL218285	CH230-89F
BM388754	UI-R-D20-
BF151027	uy91d04.x
AA544572	v167b12..r
B1064111	B1064111
BB481139	BB481139
I13597000	v167b12..x

polylinker.	Site-1:	Not I;	Site-2:	Eco RI; 1st strand cDNA
	was prepared from human tonsillar cells enriched for			
	germinal center B cells by flow sorting (CD20+, IgD+),			
	provided by Dr. Louis M. Strandt (NCI), Dr. David Allman			
	(NCI) and Dr. Gerald Matti (CSBR). cDNA synthesis was			
	primed with a Not I - oligo(dT) primer			
	[5'-TGTTACCAATCTCAAGTCGGAGCGGCCGCATTTTTTTTTTTT-3'			
]. Double-stranded cDNA was ligated to Eco RI adaptors			
	(Pharmacia), digested with Not I and cloned into the Not I			
	and Eco RI sites of the modified pTV73 vector. Library			
	went through one round of normalization, and was			
	constructed by Bento Soares and M. Fatima Bonaldo."			

BASE COUNT	147 a	129 c	144 g	134 t	1 others
ORIGIN					

Query Match	99.8%; Score 554; DB 9; Length 555;
Best Local Similarity	100.0%; Pred. No. 4.1e-108;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

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Db	1	TTTTTTTTCTTTAAATAACAATTGGAAAAAGGTGAAGAAAATCCTTAAGAAGGTATGG	60
Oy	61	aggcagatgtccacagcctgcatttcagttcacagaactgtccaccagagcgttcgatgaact	120
Db	61	AGGCCAGATGTCCACAGCTCATTCAGTTCACAGAACTGTCCACAGACTTCATCAGAACT	120

1

LOCUS	AA747315	555 bp	mRNA	linear	EST 17-MAR-1991
DEFINITION	nr886d2.s1 NCI- <i>CGAP</i> - <i>GCBI</i> Homo sapiens cDNA clone IMAGE:1269315 3', mRNA sequence.				
ACCESSION	AA747315				
VERSION	AA747315.1	GI:2787273			
FEATURES					

SOURCE

DEPENDENT

AUTHORS

1

JOURNAL,

FEATURES

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2002, 10:53:56 ; Search time 6963.4 Seconds
(without alignments)
1075.740 Million cell updates/sec

Title: US-09-853-544-1

Perfect score: 555
Sequence: 1 ttttttttcttaataac.....agttgtcagcgttcgcaca 555

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gp_estl:*
10: gp_estl2:*
11: gp_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	99.8	555	9	AA747315
2	470.6	84.8	563	9	AA747315
3	446.4	80.4	782	10	BF525647
4	444.6	80.1	515	10	BF739767
5	415.6	74.9	422	10	BF436003
6	412.2	74.3	454	9	AI392801
7	402.6	72.5	425	9	AA148983
8	394.4	71.1	455	9	AI697980
9	369.8	66.6	437	9	AA295170
10	364.4	65.7	409	9	AI283647
11	317.8	57.3	343	9	AA687243
12	310.6	56.0	332	9	AI393927
13	265.2	47.8	415	10	HA4044
14	250.2	45.1	432	10	BF754185
15	249	44.9	285	9	AI783873
16	240.2	43.3	400	10	HA4117
17					HA4117 y073e04.r1

18	240	43.2	245	10	R70141
19	213	38.4	248	9	AI918219
20	178	32.1	580	9	BE110202
21	173.6	31.3	414	10	BF401780
22	168.6	30.4	397	10	BI403166
23	168.6	30.4	504	9	BE114223
24	168.4	30.3	585	10	BF416269
25	167.2	30.1	399	10	BI119093
26	165.4	29.8	635	10	BF404955
27	160.4	28.9	578	12	A2488750
28	156.8	28.3	708	9	BI138537
29	151	27.2	513	10	BM195829
30	133	24.0	452	9	AI741034
31	90.6	16.3	238	10	BF402467
32	78	14.1	239	10	BE241758
33	78	14.1	282	10	BM193296
34	78	14.1	554	10	BM146800
35	72.2	13.0	753	9	BO098875
36	69.6	12.5	617	10	BE243742
37	65.8	11.9	622	12	BM305262
38	65.8	11.9	748	12	BM339028
39	64.4	11.6	740	12	CNS02XF8
40	64.2	11.6	692	10	BM388754
41	59.2	10.7	298	10	BF151027
42	58.2	10.5	254	9	AA544572
43	57	10.3	640	10	BU064111
44	55.8	10.1	179	9	BA481139
45	54.2	9.8	243	9	AI597000

ALIGNMENTS

RESULT 1
LOCUS AA747315 555 bp mRNA linear EST 17-MAR-1999
DEFINITION nx886d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269315 3',
mRNA sequence.
AA747315
AA747315.1 GI:2787273

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 555)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

COMMENT
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonafide, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bhrp/image/image.html
Insert Length: 888 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerisham
High quality sequence stop: 483.
Location/Qualifiers

FEATURES
source
1..555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT713D-Pac (Pharmacia) with a modified

Source	Organism	Human
REFERENCE	1 (bases 1 to 782)	
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L14M9783 row: P column: 15 High quality sequence stop: 599.	
FEATURES	location/Qualifiers	
source	1..782	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:4212734"	
	/clone_id="NCI CGAP Brn64"	
	/tissue_type="glioblastoma with EGFR amplification"	
	/lab_host="DH10B (T1 phage-resistant)"	
	/note="Organ: Brain; Vector: PCMV-SPORT6; Site_1: NCI; Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."	
BASE COUNT	186 a 216 c 204 g 174 t 2 others	
ORIGIN		
Query Match	80.4%; Score 446.4; DB 10; Length 782;	
Best Local Similarity	94.9%; Pred. No. 3.6e-85;	
Matches	525; Conservative 0; Mismatches 22; Indels 6; Gaps 6	
OY	1 ttttttctttaatacaatttgacaaaagggtgaagaatccctaacaagtatg 60	
Db	713 ttttttgcctgtatttcacaaattgacaaaagggtgaagaatccctaacaagtatg 655	
OY	61 aggcagagctcagcgtcgtatcattcaatcagaactgtccctagaagcttga- 119	
Db	654 agccacaggtcca-ctctgattcaggttcacacaaactgtctcagagcgttggaac 596	
OY	120 tggaaatgtgtaatactcagaagaagaacagggagacttagtcagagagagacagt 179	
Db	595 tggaaatgcgtattatttncagaaag-taccagagagacttactgcagacagagacagt 537	
OY	180 gtgagcgggcaacagcatccttagtct-ttcattattatatagtatattttcta 238	
Db	536 gtggacggggcaacacatccttagtctgcttattattattatgattttttcna 477	
OY	239 tatatatattatattttacatccaggtatccaggtatctgtacatctcccaaggga 298	
Db	476 tatatatattattattttttacatccaggtatccaggtatctgtacatctcccaaggga 417	
OY	299 gacatgggtgtctcccaaggcagagcaagaaggtttagcagaggaaggcagcagcgt 358	
Db	416 gacatgggtgtctcccaaggcagagcaagaaggtttagcagaggaaggcagcagcgt 357	
OY	359 gcaagcttgaggcttgctcacaagaagcttgcagagccttcagcagctgtlaagaaggcccg 418	
Db	356 gcagcctggggcttggtgcacagaagctgcagagacttcagcagcgttaagaggcccg 297	
OY	419 ggcctcgcagacgcaggtact-gagncaaagcagctcctccagctccagcccgctg 477	
Db	296 ggcctcgcagacgcaggtactgcagcagcaaacacagctcctccagctccagcccgctg 237	
OY	478 cgatcacacgctcttcgcaaatctatcatcagaggcccgcttcatgtcagaccag 537	

Db	226	CGATCCACGGCCTTCTCCGCAAACTTCATCATCATCAGGCGGCCGCTTGATGCATCCAG	177
Oy	538	cttgcagcgtgc	550
Db	176	TGTGTACAGCTGC	164
RESULT	4		
LOCUS	Bf739767	515 bp	mRNA
DEFINITION	huh9bil.x1 NCI CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3174117 3'		linear EST 10-JAN-2001
ACCESSION	Bf739767		
VERSION	Bf739767.1	GI:12066443	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Hominidae; Homo.		
REFERENCE	NCI/NINDS CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
AUTHORS	1 (bases 1 to 515)		
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCGP), Tumor Gene Index		
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Robert Jenkins, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima Bonaldo, Ph.D		
COMMENT	cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNLN DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN, send email to: info@image.lnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 462.		
FEATURES	Location/Qualifiers		
Source	1..515		
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	/clone_lib="NCI CGAP_Brn41"		
	/tissue_type="Oligodendroglioma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: brain; Vector: pTr73D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAACTGAAGTGGGAGCGGCGAATCACTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTr73 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."		
RASE COUNT	153 a	105 c	125 g 132 t
ORIGIN			
Query Match	Best Local Similarity	80.1%; Score 444.6; DB 10; Length 515;	
Matches	461; Conservative	0; Mismatches 10; Indels 1; Gaps 1;	
Oy	1	ttttttctttaataacaatttgacaaaagggtgaagaatccctaacaagtattg	60
Db	44	TTTTTTTTCTTAATAATTAACAATTGACAAAAGSGTGAAAAAATCTTAACAAGGTAATG	103
Oy	61	agggcagtgctcaggcgcatcagttcaacagaactgtccctcaggagcgttcgatgaa	120
Db	104	AGGCCAGTGTCCAGGCTCATTCATTCACAAAACCTGCTCCACAGACGCTTGATGAACT	163
Oy	121	ggaaatgtgtataatatcaagaagaagaacaggagaccttaagtcgagagagagagagctg	180
Db	164	GGAATGTGTATAATTAACAAGAAAACAGGAGGACTTAGTGCAAAAGAGAAGAGAGTG	223

QY 181 tggacgggcacacagcatccttagcttccatattatataatggtatatttctata 240
|||||
Db 224 TGACAGGGGACAGACATTCCTTACTTTCATATTATATATGATATATTTCTATA 263
QY 241 tatatttatattatattacatccaggtatccagtcacatctgtacattccaggaga 300
|||||
Db 284 TATATATTTATATATTTTACATCCAGGTATCCAGTCATCTGTACCATTTCCACAGGAGA 343
QY 301 catgagtgcttccaaggcagagaaagggttagcagggagggagggagcagcgttc 360
|||||
Db 344 CATGGTGTCTTCCAGAGCGAGACAGAAAGGTTAGCGAGGAGGCGACGACGCTGC 403
QY 361 aggcctgggcttggctcacagaagctgcagagcttcagcagcttgaagaagggcccgag 420
Db 404 AGCGTGGGGGTTGGCTCACAGAGCTGCAGAGACTTTCAGGACTGTAAAGAGGCCCGCGG 463
QY 421 ctccgacagagcaggtact-gagncaaagccagtcctccagctccagcgc 471
|||||
Db 464 CTCGCGAGAGCGCAGGTACTGCGAGCAAGCCAGTCTCTCAGCTCCAGCCGCC 515

RESULT 5
BF436003 422 bp mRNA linear EST 19-JAN-2001
LOCUS nabs2c01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:3267456 3', mRNA sequence.
ACCESSION BF436003
VERSION BF436003.1 GI:11448318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 422)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rt@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers

FEATURES
source 1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3267456"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7TD-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740959 Subtraction by Bento
Soares and M. Fatima Bonaldi."

BASE COUNT 121 a 80 C 115 g 106 t
ORIGIN

Query Match 74.9% Score 415.6; DB 10; Length 422;

Best Local Similarity 99.1%; Pred. No. 1,3e-78;
Matches 418; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 tttttttaaataaattgacaaaagggtgaagaatcccaacaagattatgagc 64
|||||
Db 1 TTTTCTTTTAAATTAACAAATTTGACAAAGGCTGAAGAAATCCATAACAAGGTATTTAGGC 60
QY 65 cagtcgcagcgcgcacatcagttcacagaacgtccctcagagcgttcgtgaactgga 124
|||||
Db 61 CAGTGTCCAGGCTGCAGTTTACATTCAGTTCACAGAACTCTCTCAGAGCTTGATGGAACTGGAA 120
QY 125 atgtgtataattacagaagaataacaggagagcttagtcagagaggagacagtgtaga 184
|||||
Db 121 ATGTGTATTAATTAACAAATAAAACAGGAGGAGCTTGTGTCAGAGAGACTACTGTGTGA 180
QY 185 cgggacaagcagatcccttagcttcttatattatattatgtatatttccatataata 244
|||||
Db 181 CGGCAACAGCATCCCTTAATGTCTTCAATTTATATATGATATATGATTTTCTATATATA 240
QY 245 tatataataattacatccaggtatccagtcacatctgtacattccaggagaacatg 304
|||||
Db 241 TATCTATATATTTTACATCCAGGTATCCAGTCATCTGTACATTTCCAGGAGACATG 300
QY 305 ggtgtctccaaggcagagacagaagaagggttaaggcagggagggcagcgatgcagc 364
|||||
Db 301 GGTGCTTCCAGGCGAGACAGCAAGGCTTAGGCAAGGGGCGACGATGTCAGGC 360
QY 365 tggggcttggctccacagaagctgcagagacttcagagctgttaagaaggcccgagctcc 424
|||||
Db 361 TGGGCTTGCTGCACGAAGCTGCGAGACCTTCAGCACTTAAAGAGGCCCGGGCTTC 420
QY 425 gc 426
Db 421 GC 422

RESULT 6
A1392901 454 bp mRNA linear EST 30-MAR-1999
LOCUS tg10e07.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2108388 3',
DEFINITION mRNA sequence.
ACCESSION A1392901
VERSION A1392901.1 GI:4222448
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 454)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rt@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1175 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
/clone_image="2108388"
/clone_lib="NCI_CGAP_CL11"
/tissue_type="B-cell, chronic lymphocytic leukemia"

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Insert Length: 615 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 455
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/clone="IMAGE:2341562"
/clone_lib="NCI-CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI-CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo.
BASE COUNT 136 a 80 c 108 g 130 t 1 others
ORIGIN
Query Match 71.1%; Score 394.4; DB 9; Length 455;
Best Local Similarity 98.1%; Pred. No. 4,3e-74;
Matches 409; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 ttttttttcttaatacaatttgacaaagggtgaagaatcctaacaagttatg 60
DB 40 ttttttttcttaatacaatttgacaaagggtgaagaatcctaacaagttatg 99
QY 61 aggcagtgctccaggtgcatcagtcacagaactgctccagagcttgatggaact 120
DB 100 AGCCAGGTGCTCCAGCGCTGATTGACAAAGTCTCCTCAGGACGTTGATGGA 159
QY 121 ggaatggttatataacagaagaaggagagagcttagtgcagagaaggagagagtg 180
DB 160 GGAATGCTATATATTACAGAAAAACAGGAGGAGCTTAGTGCANAGAGAGACAGTG 219
QY 181 tgaaggggaacagacaccccttagtcttcataattatataatgatatatttcata 240
DB 220 TGACGCGGACAGCATCTTACTCTTATATATATATGATATATATTTTCTATA 279
QY 241 tatatatatatattatcatcaccaggtatccagcatctgtaccattccaggagaga 300
DB 280 TATATATATATATATTTTACATCCAGGTATCCAGCATCTGATCATTTTCCCA -GGATA 338
QY 301 catggtgcttccaagggcagagaaaggttaagcaggaaggagcagcagctg 360
DB 339 CATGGGTGCTTCCAAAGGACAGAGAAAGGTTAAGGAGGAGGAGGAGCGACGCTGC 398
QY 361 aggcctggagctggctcacagaagctgcagagagcttcacagactgtgaagagccccc 417
DB 399 AGGCTGGGCTTGCTGCACAGAACTGCAAGAGCTTACAGCACTGTAAAGAGGCCCC 455

RESULT 9
AM295170 437 bp mRNA linear EST 16-JAN-2000
LOCUS
DEFINITION UI-H-B12-alc-d-03-0-UI.s1 NCI-CGAP_Sub4 Homo sapiens CDNA clone

IMAGE:2728733 3', mRNA sequence.
AM295170
AM295170.1 GI:6701806
EST.
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 437)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html The following repetitive
elements were found in this cDNA sequence: 269-314, >(TA
)n\$Simple-repeat
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1. 437
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2728733"
/clone_lib="NCI-CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI-CGAP_Sub4 library is a subtracted library derived from
the NCI-CGAP_Sub2 library which is a subtracted library
derived from the NCI-CGAP_Sub1 library, which is a
mixture of 21 normalized or subtracted NCI-CGAP
libraries: NCI-CGAP_C04, NCI-CGAP_Pr22, NCI-CGAP_Pr28,
NCI-CGAP_C010, NCI-CGAP_C016, NCI-CGAP_Kid5,
NCI-CGAP_Kid12, NCI-CGAP_Kid3, NCI-CGAP_Kid11,
NCI-CGAP_Lym2, NCI-CGAP_Br2, NCI-CGAP_C08, NCI-CGAP_C11L1,
NCI-CGAP_L612, NCI-CGAP_Br23, NCI-CGAP_Lu5,
NCI-CGAP_Lu24, NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6,
NCI-CGAP_Br25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI-CGAP_Kid3 pool 1 : LHAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 1323376-1323911,
1456008-1456775, 1500552-1502855) NCI-CGAP_Kid5 pool 1 :
LHAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
1323912-1325831, 1471368-1472993, 1492104-1493255)
NCI-CGAP_Lu5 pool 1 : LHAM 3575-3582, 3851-3854 (IMAGE
Clonoids 1414920-1417991, 1520904-1522439) NCI-CGAP_GC4
pool 1 : LHAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI-CGAP_Pr22 pool 1 : LHAM 2457-2459, 2758-2759,
3062-3068 (IMAGE Clonoids 985608-986759, 1101199-1101959,
1217928-1220615) NCI-CGAP_C010 pool 1 : LHAM 2644-2653,
2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351)
) Subtraction was performed as previously described
(Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6, 791-806.)
TAG_Lib=NCI-CGAP_GC4
TAG_NISSUE=germ cell
TAG_SEQ=AAATC

BASE COUNT
ORIGIN

126 a 73 c 102 g 136 t

strand cDNA was primed with a Not I - oligo(dt) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA

Query Match	65.78%	Score 364.4	DB 9	Length 409
Best Local Similarity	99.58%	Pred. No. 1,1e-67		
Matches 365	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Oy	1	tttttttctttaaataacaatttgcacaaagggttgaaagaaaccttaacaagaatttg	60
Db	43	TTTTTTTTCTTTAATAACAAATTTTGACAAAGGGTGAAGAAATCTTAACAAGATTG	102
Oy	61	aggccagtgcccaagcgtgcattcagltcaacagaactgttcctcagaacgtltgcatggaact	120
Db	103	AGGCGACGTTCCAGGCGTCCATTCATTCACAAACGTTCTCAGGACGTTGCATGGAACT	162
Oy	121	ggaaatcgtgtataataatacagaagaacaaacagggaggaacttagtcgcagagagggagacgacg	180
Db	163	GGAATGTGTATTAATTACAGAAAGAAACACGGAGACCTTAGTCAGAGAGGAGACAGAGTG	222
Oy	181	ttggcagggcacaacagatccttagtccttccattttatataatagatgatatttttttata	240
Db	223	TGGACGGGCAACAGCATCTCTTAGTCTTTTCATATTATATATGGMATATGTATTTCATANA	282
Oy	241	tataattatataatttcaacatccacagatataccacgtacatcgtlaccatttcccaaggagaa	300

QY	301	cattggtctcccaaggcgagacagaaggttaggcaggaagggcagcgcagtgc	360
Db	343	CATGGTCTCTTCACAGGCGAGACAGAAAGGTTAGCGGGAAGGGGCAGCACGCTGC	402
OY	361	agacttgg	367
Db	403	AGGCTTG	409

RESULT	11			
AA687243				
LOCUS	AA687243	343 bp	mRNA	linear
DEFINITION	nv609092.1 NC1_CGAP_GCB1	Homo sapiens	cDNA	EST 24-DEC-1991
	mRNA sequence.			clone IMAGE:1334226 3'
ACCESSION	AA687243			
VERSION	AA687243.1	GI:2675434		
KEYWORDS	EST.			

VERSION	AA687243.1	GI:2675434
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 343)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsb@mail.nih.gov unknown library type	
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	Seq primer: -40m13 fwd. ET from Amersham	

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    /db_xref="taxon:9606"
    /clone_image="1234226"
    /clone_lib="NCI_CGAP_GCB1"
    location/qualifiers
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      Seq primer: 40ml3 fwd. ER from Amersham
      High quality sequence stop: 329.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2002, 15:17:46 ; Search time 190.69 Seconds
(without alignments)
714.912 Million cell updates/sec

Title: US-09-853-544-1

Perfect score: 555
Sequence: 1 ttttttttttctaataac.....agtgtgcagcgtgcgaca 555

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, NA: *
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCITUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	7.5	7218	1	US-08-232-463-14
2	38.8	7.0	2875	5	PCR-US93-06251-63
3	36.8	6.6	71989	4	US-09-443-501A-2
4	35.8	6.5	3777	3	US-09-121-321-15
5	35.8	6.5	3777	4	US-08-933-803A-15
6	35.2	6.3	6769	1	US-08-480-784-20
7	35.2	6.3	6769	1	US-08-483-553-20
8	35.2	6.3	6769	1	US-08-487-003-20
9	35.2	6.3	6769	1	US-08-483-554B-20
10	35.2	6.3	6769	1	US-08-488-011B-20
11	35.2	6.3	6769	4	US-08-850-727-20
12	35.2	6.3	6769	5	PCR-US95-10202-20
13	35.2	6.3	6769	5	PCR-US95-10203-20
14	35.2	6.3	6769	3	PCR-US95-10220-20
15	35.2	6.3	68750	3	US-09-335-409-1
16	35.2	6.3	68750	4	US-09-568-102-1
17	35.2	6.3	68750	4	US-09-567-969-1
18	35.2	6.3	68750	4	US-09-568-480-1
19	35.2	6.3	68750	4	US-09-568-486-1
20	35.2	6.3	68750	4	US-09-568-472-1
21	34.2	6.2	1420	1	US-08-589-981-1
22	34.2	6.2	2689	2	US-08-985-090-1
23	34.2	6.2	2689	3	US-09-165-543-1
24	34.2	6.2	2699	3	US-09-167-354-5
25	33.8	6.1	600	4	US-08-998-416-228
26	33.8	6.1	2028	4	US-09-634-920-1
27	33.8	6.1	2734	3	US-09-135-021-79

28	33.8	6.1	2821	4	US-09-135-021A-115	Sequence 115, App
29	33.8	6.1	3181	3	US-09-135-021-1	Sequence 1, Appl
30	33.8	6.1	3181	4	US-09-135-020-1	Sequence 1, Appl
31	33.8	6.1	3181	4	US-09-135-021A-1	Sequence 1, Appl
32	33.8	6.1	3182	3	US-09-135-021-5	Sequence 1, Appl
33	33.6	6.1	5526	3	US-08-751-359-21	Sequence 21, Appl
34	33.6	6.1	5526	4	US-08-907-146-21	Sequence 21, Appl
35	33.2	6.0	1789	1	US-08-455-543A-29	Sequence 29, Appl
36	33.2	6.0	1789	2	US-08-223-305C-29	Sequence 29, Appl
37	33.2	6.0	2338	1	US-08-455-543A-31	Sequence 31, Appl
38	33.2	6.0	2338	2	US-08-223-305C-31	Sequence 31, Appl
39	33.2	6.0	5904	1	US-07-745-206A-6	Sequence 6, Appl
40	33.2	6.0	5904	1	US-08-455-543A-3	Sequence 3, Appl
41	33.2	6.0	5904	2	US-08-193-078B-3	Sequence 3, Appl
42	33.2	6.0	5904	2	US-08-223-305C-3	Sequence 3, Appl
43	33.2	6.0	5904	2	US-08-223-305C-3	Sequence 3, Appl
44	33.2	6.0	5904	2	US-08-149-097D-3	Sequence 3, Appl
45	33.2	6.0	6575	3	US-08-311-363-6	Sequence 6, Appl
					US-08-949-386-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

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	Best Local	Similarity	2.9%,	Pred.No.0.081,						
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QY	14	aataacaatttcgacaaagggtgaagaatccctaacaaggtatctgaagccagtgcaca	73							
Db	1451	ATAGAAAGATTGTTACRRR	1392							
QY	74	ggctcaltccagttcacagaactgtccccaagcttgcatygaactygaatytgtata	133							
Db	1391	RRR	1332							
QY	134	attacaagaagaacagaggagcttaagcaagaagagacagatgytgcaggcgaca	193							
Db	1331	RRR	1272							
QY	194	gcatccttagtcttcataattatalataytatgatatttcatalatatattatat	253							
Db	1271	RRR	1212							
QY	254	atttaacctcgaagtatacccagtcactcgtaaccattccccaggvgagactygvtctcc	313							
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QY	314	aagcgagacagaaagggttagcagagaaaggcagcagactgtcagctcggggcttg	373							
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QY	374	gtctcacagaagctgcagagag	393							
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PCT-US93-06251-63
;
; Sequence 63, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-06251-63

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Best Local Similarity 47.5%: Pred. No. 0.31;
Matches 115; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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OY      117      aactggaatctgtataatcacagaagaacaagggaagacttagtgcagaagaagacg 176
Db      1731     AAAAGAAACTGAGATTAATTTTAGAAGAAATGAACGAGAGATTAGCATGGAACATGGAA 1790

OY      177      agtgtgagcagggaacagacatcccttagtccttcataattatataatgatatgtcttc 236
Db      1791     AGAGAAATCAATCCACGAGCAAGTTTATATACAAATTTTAAATATGGTAAAGCTTTACT 1850

OY      237      tatatatattatataatttacaatccagatccagatccctgtaccattccag 296
Db      1851     TTGAAATGATAAATTTCTATGTTTAGTGTGTACTTAACCTGTATGTTGAACATGTGCTATG 1910

OY      297      ga 298
Db      1911     CA 1912

RESULT      3
US-09-443-501A-2/C
; Sequence 2, Application US/09443501A
; Patent No. 6103342
; GENERAL INFORMATION:
; APPLICANT: Kosan Biosciences, Inc.
; APPLICANT: Julien, Bryan

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QY	DB	Query Match	Best Local Similarity	Matches	68; Conservative	Score	36.8; Pred. No.	DB	4; Length	71989;	DB	486	CGCCTTCGCGAAACATCATCATCATCATCAGGCGCGCTTCATGTCGATCCAGTGTGCGAG	545	18053	CGCGGTAGCGCGTACGTACCGGAGAGCGCGGCTGTGGTGAACCGCGTGTGTCGAG	17994
QY	DB	426	18113	CAGCTCCCGATGCTATGCCACACAGGAGCTCCGCGCTTTCAGCCCCACGACGCGACAG	18054	6.6%;	56.2%;	0;	Mismatches	53;	Indels	0;	Gaps	0;			
QY	DB	486	CGCCTTCGCGAAACATCATCATCATCATCAGGCGCGCTTCATGTCGATCCAGTGTGCGAG	545	6.6%;	36.8;	DB	4;	Length	71989;							
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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3     APPLICATION NUMBER: US 08/483,554
4     FILING DATE: 07-JUN-1995
5 PRIOR APPLICATION DATA:
6     APPLICATION NUMBER: US 08/348,824
7     FILING DATE: 29-NOV-1994
8 PRIOR APPLICATION DATA:
9     APPLICATION NUMBER: US 08/308,104
10    FILING DATE: 16-SEP-1994
11 PRIOR APPLICATION DATA:
12    APPLICATION NUMBER: US 08/300,266
13    FILING DATE: 02-SEP-1994
14 PRIOR APPLICATION DATA:
15    APPLICATION NUMBER: US 08/289,221
16    FILING DATE: 12-AUG-1994
17 ATTORNEY/AGENT INFORMATION:
18     NAME: Ihnen, Jeffrey L.
19     REGISTRATION NUMBER: 28,957
20 REFERENCE/DOCKET NUMBER: 24884-109347
21 TELECOMMUNICATION INFORMATION:
22     TELEPHONE: 202-962-4810
23     TELEFAX: 202-962-8300
24 INFORMATION FOR SEQ ID NO: 20:
25     SEQUENCE CHARACTERISTICS:
26         LENGTH: 6769 base pairs
27         TYPE: nucleic acid
28         STRANDEDNESS: double
29         TOPOLOGY: linear
30 MOLECULE TYPE: DNA (genomic)
31 HYPOTHETICAL: NO
32 ANTI-SENSE: NO
33 ORIGINAL SOURCE:
34     ORGANISM: Homo sapiens
35 US-08-850-727-20
36
37 Query Match          6.3%; Score 35.2; DB 4; Length 6769;
38 Best Local Similarity 58.7%; Pred. No. 4.4;
39 Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0.
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42           | | | | | | | | | | | | | | | | | | | | | | | | | |
43 Db      1206 tatgttatatatatcatatcatatcatatcatatcatatcatatcatat 1147
44
45 Oy      264   caggtatcccgagtcactcgtaccattcccgaggagacatggagt 307
46           | | | | | | | | | | | | | | | | | | | | | | | | | |
47 Db      1146 tataatatatatatgatgtaatccacaccttgtagtatatgttgt 1103
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49 RESULT 12
50 PCT-US95-10202-20/c
51 Sequence 20, Application PC/TUS9510202
52 GENERAL INFORMATION:
53 APPLICANT: Shatluck-Eldems, Donna M.
54 APPLICANT: Simard, Jacques
55 APPLICANT: Emi, Mitsuru
56 APPLICANT: Nakamura, Yusuke
57 APPLICANT: Durocher, Francine
58 TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
59 TITLE OF INVENTION: In the 17q-linked Breast and Ovarian Cancer
60 NUMBER OF SEQUENCES: 85
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
63 STREET: 1201 New York Avenue, N.W., Suite 1000
64 CITY: Washington
65 STATE: DC
66 COUNTRY: USA
67 ZIP: 20005
68 COMPUTER READABLE FORM:
69 MEDIUM TYPE: Floppy disk
70 COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
FAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10202-20

Query Match
Best Local Similarity 6.3%; Score 35.2; DB 5; Length 6769;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0.

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RESULT 13
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Sequence 20, Application PC/TUS9510203
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Mikl, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer

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? TITLE OF INVENTION: Susceptibility Gene
? NUMBER OF SEQUENCES: 85
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
? STREET: 1201 New York Avenue, N.W., Suite 1000
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/10203
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US
? FILING DATE: 07-JUN-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/409,305
? FILING DATE: 24-MAR-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/348,824
? FILING DATE: 29-NOV-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08-308,104
? FILING DATE: 16-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/300,266
? FILING DATE: 02-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/289,221
? FILING DATE: 12-AUG-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Ihnen, Jeffrey L.
? REGISTRATION NUMBER: 28,957
? REFERENCE/DOCKET NUMBER: 24884-109347
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-962-4810
? TELEFAX: 202-962-8300
? INFORMATION FOR SEQ ID NO: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 6769 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
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? GENERAL INFORMATION:
? APPLICANT: Skolnick, Mark H.
? APPLICANT: Goldgar, David E.
? APPLICANT: Miki, Yoshio
? APPLICANT: Swenson, Jeff
? APPLICANT: Kamb, Alexander
? APPLICANT: Harshman, Keith D.
? APPLICANT: Shattuck-Eidens, Donna M.
? APPLICANT: Tavtigian, Sean V.
? APPLICANT: Wiseman, Roger W.
? APPLICANT: Futreal, P. Andrew
? TITLE OF INVENTION: Method for Diagnosing a
? TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
? NUMBER OF SEQUENCES: 85
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
? STREET: 1201 New York Avenue, N.W., Suite 1000
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/409,305
? FILING DATE: 24-MAR-1995
? PRIOR APPLICATION DATA:
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? FILING DATE: 29-NOV-1994
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? FILING DATE: 16-SEP-1994
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? APPLICATION NUMBER: US 08/300,266
? FILING DATE: 02-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/289,221
? FILING DATE: 12-AUG-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Ihnen, Jeffrey L.
? REGISTRATION NUMBER: 28,957
? REFERENCE/DOCKET NUMBER: 24884-109347
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-962-4810
? TELEFAX: 202-962-8300
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? SEQUENCE CHARACTERISTICS:
? LENGTH: 6769 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
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? HYPOTHETICAL: NO
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? ORGANISM: Homo sapiens
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Best Local Similarity 58.7%; Pred. No. 4.4;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	531.6	95.8	1562	22 ABA15366 Human nervous syst
C 2	531.6	95.8	1562	22 ABA15367 Human nervous syst
C 3	531.6	95.8	1562	22 AAS27703 DNA encoding novel
C 4	531.6	95.8	1562	22 AAS27706 DNA encoding novel
C 5	531.6	95.8	4169	22 AAH77992 Nucleotide sequenc
C 6	528.4	95.2	1002	22 AAH99684 Human protein enco
C 7	77.6	14.0	272	22 ABA11460 Human nervous syst
C 8	63	11.4	5241	22 AAH77993 Nucleotide sequenc
C 9	43.2	7.8	557	22 AAH10423 Human cDNA clone (

C 10	43.2	7.8	2763	22 AAH17538 Human cDNA sequenc
C 11	40.2	7.2	1599	23 ABL08153 Drosophila melanog
C 12	40.2	7.2	6229	23 ABL08152 Drosophila melanog
C 13	39.6	7.1	2914	22 AAK70730 Human immune/haema
C 14	39	7.0	15548	22 ABL34155 Human immune syste
C 15	38.8	7.0	2888	11 AAO03743 Human SKI related
C 16	38.6	7.0	6754	22 AAS61304 Human gene regulat
C 17	38	6.8	14061	23 ABL03359 Drosophila melanog
C 18	38	6.8	16602	22 ABL32727 Human immune syste
C 19	37.4	6.7	1140	22 ABL17181 Human zyxine fragm
C 20	37.4	6.7	1716	22 AA171755 Human zyxine codin
C 21	37.4	6.7	2217	22 ABA82698 zyxin gene SEQ ID
C 22	37.4	6.7	2320	21 AAF21879 Human breast and o
C 23	37.4	6.7	3675	23 ABL14664 Drosophila melanog
C 24	37.4	6.7	4320	23 ABL04688 Drosophila melanog
C 25	37.4	6.7	21311	23 ABL04750 Drosophila melanog
C 26	37.2	6.7	5379	24 ABL33677 Human immune syste
C 27	37.2	6.7	5379	24 ABL34577 Human metastasis a
C 28	37.2	6.7	138169	21 ABA34791 Human adenosine re
C 29	37.2	6.7	14189	21 AAF20913 Human ELAM-1 polyn
C 30	37.2	6.7	14189	21 AAF21127 Human low adenosin
C 31	37.2	6.7	14189	21 AAF21152 Human low adenosin
C 32	37.2	6.7	14189	21 AAA35005 Human adenosine re
C 33	37.2	6.7	14189	21 AAA35030 Human adenosine re
C 34	37.2	6.7	146981	21 AAF21442 Human ELAM-1 polyn
C 35	37.2	6.7	209273	21 AAF21437 Human factor-relat
C 36	37	6.7	1341	21 AAC76115 Human ORFX ORF1670
C 37	36.8	6.6	71989	21 AAA29349 Sorangium cellulosa
C 38	36.6	6.6	1877	22 AAS02381 Brassica napus DNA
C 39	36.6	6.6	5379	24 ABL33676 Human immune syste
C 40	36.6	6.6	5379	24 ABL34576 Human metastasis a
C 41	36.6	6.6	32190	22 AAS29937 Human lung antigen
C 42	36.6	6.6	113515	24 ABL34174 Human immune syste
C 43	36.4	6.6	10553	22 ABA16395 Human nervous syst
C 44	36.4	6.6	10553	22 AAK69113 Human immune/haema
C 45	36.2	6.5	3730	22 ABA19745 Human nervous syst

ALIGNMENTS

RESULT 1	ABAI5366/C	ABAI5366 standard; DNA: 1562 BP.
ID	ABAI5366	
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AC		
XX		
DT	23-JUN-2002 (first entry)	
XX		
DE	Human nervous system related polynucleotide SEQ ID NO 7697.	
XX		
KW	Human; noctropic; neuroprotective; cytosolic; dermatological; vlrucide;	
KW	Immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;	
KW	antiparkinsonian; antischizic; antianaemic; antilarthritic; cancer;	
KW	antirheumatic; hepatotropic; cerebroprotective; antinflammatory;	
KW	antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;	
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;	
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.	
XX		
OS	Homo sapiens.	
PN		
XX	WO200159063-A2.	
PD		
XX	16-AUG-2001.	
XX		
PF	17-JUN-2001; 2001WO-US01334.	
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PR	31-JAN-2000; 2000US-0179065.	
PR	04-FEB-2000; 2000US-0180628.	
PR	24-FEB-2000; 2000US-0184664.	
PR	02-MAR-2000; 2000US-0186350.	
PR	16-MAR-2000; 2000US-0189874.	
PR	17-MAR-2000; 2000US-0190076.	

CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 1562 BP: 311 A; 529 C; 423 G; 299 T; 0 other;

Query Match 95.8%; Score 531.6; DB 22; Length 1562;
 Best Local Similarity 98.9%; Pred. No. 4,9e-133;
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RESULT 2
 ID ABA15367/C
 AC ABA15367;
 DT 23-JAN-2002 (first entry)
 DE Human nervous system related polynucleotide SEQ ID NO 7698.

XX Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; antiviral;
 KW antiparkinsonian; antischistosomal; antianaemic; antithrombotic; cancer;
 KW antihemorrhagic; hepatoprotective; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiliver; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephroprotective; gene therapy; vaccine; ds.
 XX Homo sapiens.
 XX WO200159063-A2.
 PD 16-AUG-2001.
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 PF 17-JAN-2001; 2001WO-US01334.
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 PR 04-FEB-2000; 2000US-0180628.
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 PR 16-MAR-2000; 2000US-0189874.
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 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
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 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
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 PR 05-SEP-2000; 2000US-0229509.
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 PR 06-SEP-2000; 2000US-0230437.
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PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 06-DEC-2000: 2000US-0251479.

PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251890.
PR 08-DEC-2000: 2000US-0251989.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259578.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM.
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7698; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABAI21534) and proteins
CC (ABAI4678-ABAI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1562 BP; 312 A; 528 C; 423 G; 289 T; 0 other;
SQ
Query Match 95.8%; Score 531.6; DB 22; Length 1562;
Best Local Similarity 98.9%; Pred. No. 4,9e-133;
Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 ttttttttcttaataacaatttgacaaaagggggaagaatcctaacaagatgac 60
DB 1514 ttttttttcttaataacaatttgacaaaagggggaagaatcctaacaagatgac 1455
QY 61 aggcacagtcacagctgcattcagtcacagaactgtccacagacgttcagtggaact 120
DB 1454 AGGCCAGTGTCCAGGCTGCATTTCACAGAACTGTCTTCAGCAGTTCATGGAAC 1395
QY 121 ggaatggtatataatcacaagaagaacagggaggaacttagtcacaaggaggaagtg 180
DB 1394 GGAATGTGTATATATACAGAAAGAGGAGGAGCTTAGTCACAGAGGAGCAGCAGTG 1335
QY 181 tgaacgggcaacagacaccccttagcttctcatattatataatgtaattatcttata 240
DB 1334 TGACGGGGCAGACGATCCCTTACTTTTCATATATATATATATATATATATATAT 1275
QY 241 tatatatatatattatcatcatccaggtatccagtcacatcgtaccattcccaaggaga 300
DB 1274 TATATATTTATATATTTTACATCCAGGTATCCAGTCACTCTGATACCATTTTCCAGGAG 1215
QY 301 catgggtgcttcccaaggcgagacagaaggggttaaggcaggaaggagcagcaggtgc 360
DB 1214 CATGGGTGCTTCCAGAGCGAGACAGGAAGGGGTAGGACAGGAGGAGCAGCAGCTGC 1155
QY 361 aggcctgggcttggtccacagaagctgcaggaagcctcaacagatgtgaagaagcccccgg 420
DB 1154 AGGCTGGGCTTGCTTCACAGAACTGCAGGAGCTTACGGAAGGAGGAGGAGGAGGAGG 1095

PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465460/50.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders
XX
XX
XX Claim 1: SEQ ID NO 1363; 880bp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II), (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative
CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), Chromosomal
CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC disorders (e.g. glomerulonephritis), cardiovascular disorders
CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC Addison's disease), reproductive system disorders, gastrointestinal
CC disorder (inflammatory disorders), liver disorders (cirrhosis),
CC as stimulators of B-cell responsiveness to pathogens, activators of
CC T-cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction
CC pathway protein coding sequences and PCR primers of the invention.
XX
XX Sequence 1562 BP; 311 A; 529 C; 423 G; 299 T; 0 other:
SQ

Query Match 95.8%; Score 531.6; DB 22; Length 1562;
Best Local Similarity 98.9%; Pred. No. 4.9e-133;

Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 tttttttcttaataacaattgacaaagggtgaagaatccctaacaaggtatcg 60
|||||
Db 1514 TTTTTCCTTAATAATTAACATTTTACAAAAGGGAAGAAATCTTAACAAGATATG 1455
QY 61 aggcacagtgctcagcgtcattcagtcacagaactgtccccaagcgttcagtaact 120
|||||
Db 1454 AGGCCAGTGTCCAGGCTGATTCAGTTACAGAACTGCTCCAGACGTTGATGAGACT 1395
QY 121 ggaatggtataataatacaagaagaagggaaggttagtcagagagagagagagtg 180
|||||
Db 1394 GGAAATGTATATATTAATTAAGAAAGAAAGGAGGAGCTTAGTACAGAGAGAGACAGTG 1335
QY 181 tgaacgggaacaagcaactccttagcttcattatataatgataatgataatgata 240
|||||
Db 1334 TGGACGGGCAACAGCATCTTACTGTTTATATATGATATATATTTCTATA 1275
QY 241 tatatatatatattatcatcaccaggtatccagtcacatgtaaccattcccaaggaga 300
|||||
Db 1274 TATATATTTATATATTTATCATTCACAGGTATCCAGTCACTGTACCATTTCCAGGAGA 1215
QY 301 catggtgtctccaaagcgagagacaggaagggttagtcagagagagagagagagtg 360
|||||
Db 1214 CATGGTGCTTCCAAAGCGAGACAGGAAGGTTAAGCGAGGAAGGCGAGCGAGTGTC 1155
QY 361 aggcctgagcgttgctgcacagaagctgcagagagcttcacacagctgtaagaaggcccg 420
|||||
Db 1154 AGGCTGGGGCTTGTCCTACAGAAAGCTGACAGAGCTTACACGACTGTAAAGAGGCCCGGG 1095
QY 421 ctccgcagagcccaaggtact-gagmcaagccaagtcctccagctccagcccgctcg 479
|||||
Db 1094 CTCGCGAGAGCGCAGGTACTGCGACGAAGCCAGTCTCCACTCCACCCTCCGCTGGG 1035
QY 480 atccaccgcctctccgaacactcatcatcaagggccgctcatatgcatcaagt 539
|||||
Db 1034 ATCCACCGCCTTCTCCGAAACTTCATCATCAAGGCGCCGCTTCATGCAATCAGTT 975
QY 540 gtccagcgtgc 550
|||||
Db 974 GTGCAAGCGTGC 964
RESULT 4
AAS27706/c
ID AAS27706 standard; DNA: 1562 BP.
XX
XX AAS27706;
XX
XX 07-NOV-2001 (first entry)
XX
XX DNA encoding novel signal transduction pathway protein, Seq ID 1366.
XX
XX Neutropenictive; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory condition;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ds;
KW acquired immune deficiency syndrome.
XX
XX Homo sapiens.
OS
XX WO200154733-A1.
PN
XX 02-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US01312.
PF
XX 31-JAN-2000; 2000US-0179065.
PR

PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226865.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230436.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
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PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
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XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders
XX

PS Claim 1: SEQ ID NO 1366; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II) (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
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 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.
 XX
 XX Sequence 1562 BP; 312 A; 528 C; 423 G; 299 T; 0 other;

Query Match 95.8%; Score 531.6; DB 22; Length 1562;
 Best Local Similarity 98.9%; Pred. No. 4.9e-133;
 Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 tttttttcttaataacaattgcacaaagggtgaagaatccttaacaagatattg 60
 DB 1514 TTTTCTTTCTTAAATTAACAATTGACAAAGGTTGAAGAAATCTAAACAAGATTG 1455
 QY 61 agggccagtgtccagggtgcttcattcagtcacagacgtgctccaggagcgttgtaact 120
 DB 1454 AGGCGACGTGCTCCAGCTGATTCAGTTCAACAGAACTGCTCCAGGAGCTTGAGAACT 1395
 QY 121 ggaatgctgtataataacagaagaacaggagagcttagtcacaagaggaacagatg 180
 DB 1394 GGAAGTGTGATATATTACAGAAAGAACAGGAGGACTTAGTGCACAGAGACAGACAGTG 1335
 QY 181 tggagggcacaacagatccttagcttcaatattatataatgatatatgatttctata 240
 DB 1334 TGCACGCGCAACGACATCTTACTCTTTATATATATATATATATATATATATATAT 1275
 QY 241 tatatatatatattatattatcatccaggtatccagtcacatctfraccatttccaggaga 300
 DB 1274 TATATATATATATATTTTACATCCAGGATCCAGTCACTGTGACATTTCCACAGGAGA 1215
 QY 301 catgggtgcttccaaggcagagaagaagggtttaggcaggaggaaggagcagcaggtgc 360
 DB 1214 CAGGGTGTGCTCCAGAGCGAGACAGAAAGGTTAGGACAGGAGGAGGACGACGCTGC 1155
 QY 361 aggcctggagcttggtcacaagaagctgcaggagcttcagcagctgttaagaaggcccgag 420
 DB 1094 CTCCGACAGAGCGAGTACTGCGAGCAAAAGCCAGTCTCCAGTCCACGCCCCGCTGCG 1035
 QY 421 ctccggaagcgcaggctact-gagncaaagccagctcctccagctcagcccccctgtgg 479
 DB 1154 AGGCTGGGGCTTGCTGCACAGAACTGCAGAGACTTTCAGAGACTGTAAAGAGGCCCCGGG 1095
 QY 480 atccacgcgcttcgcgaacttcacatcatcagggcccggttcattgcatcagtt 539
 DB 1034 ATCCACGCGCTTCTCCGCAAACTTCATCATCATCAGGCCCCGCTTATGTCATCCAGTT 975
 QY 540 gtgcagcgtgc 550
 DB 974 GTGCAGCGTGC 964

RESULT 5

AAH77992/C
 ID AAH77992 standard; DNA; 4169 BP.
 XX
 AC AAH77992;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of human protein kinase SGK223.
 XX
 KW Human; protein kinase; cancer; immune disease; cardiovascular disease;
 KW brain disease; neuronal disease; Alzheimer's disease; chromosome 8;
 KW Parkinson's disease; multiple sclerosis; metabolic disorder;
 KW peripheral nervous system disease; amyotrophic lateral sclerosis;
 KW infection; ocular disease; migraine; pain; sexual dysfunction;
 KW mood disorder; attention disorder; cognition disorder; hypotension;
 KW hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3735
 FT /tag="a
 FT /product="protein kinase"
 XX
 PN WO200166594-A2.
 XX
 PD 13-SEP-2001.
 XX
 PD 02-MAR-2001; 2001WO-US06638.
 XX
 PR 06-MAR-2000; 2000US-0187150.
 PR 29-MAR-2000; 2000US-0193404.
 PR 13-NOV-2000; 2000US-0247013.
 XX
 PA (SUGEN) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 DR WPI; 2001-536777/59.
 XX
 DR P-PSDB; AAG67393.
 XX
 PT Nucleic acids capable of encoding human polypeptides having a kinase or
 PT kinase-like activity; useful for diagnosing a disease selected from
 PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Example 1; Fig 1B-C; 201ip; English.
 XX
 CC The present sequence encodes a human protein kinase. The
 CC gene is located at chromosomal position 8p22-p23. The kinase
 CC polypeptides are useful for diagnosing a disease or disorder
 CC selected from cancers (e.g. cancers of tissues and cancers of
 CC hematopoietic origin), immune-related diseases and disorders,
 CC cardiovascular disease, brain or neuronal-associated diseases (e.g.
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis),
 CC metabolic disorders, peripheral nervous system diseases, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC infections caused by bacteria, infections caused by fungi, ocular
 CC diseases, migraines, pain, sexual dysfunction, mood disorders,
 CC attention disorders, cognition disorders, hypotension, hypertension,
 CC psychotic disorders, dyskinesias, and organ transplant rejection.
 CC Kinase inhibitors are useful for treating diseases and disorders
 CC described above.
 XX
 XX Sequence 4169 BP; 871 A; 1398 C; 1167 G; 733 T; 0 other;

Query Match 95.8%; Score 531.6; DB 22; Length 4169;
 Best Local Similarity 98.9%; Pred. No. 7.6e-133;
 Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 tttttttcttaataacaattgcacaaagggtgaagaatccttaacaagatattg 60
 |||

D 4110 TTTTCTTTCTTAATFACATTTGACAAAAGGTTGAGAAATCTCTAACAAGGTATTG 4051
QY 61 aggcacagtgccagcgtgcacgtcagtcacagacagtcgtccacagacgttcacagtggaact 120
D 4050 AGGCAGTGTCCAGGCTGCATTCAGTTCACAGAAAGTGTCTCTCAGGACGTTGCAATGGAAGT 3991
QY 121 ggaatggtatataataacagaagaagaagagagactgagtcagagagagagagagagtg 180
D 3990 GGAAGTGTATATATACAGAAAGGAGGAGTGTAGTCCAGAGAGACAGAGAGT 3931
QY 181 tgaacggagcaacagcactcctagctcttcacattatataatgatatgatatgttccata 240
D 3930 TGGACGGGCAACAGCATCTCTTCTTCTATTTATATATGATATGATATTTCTATA 3871
QY 241 tatataattatataattatcatccagatccacagtcacatctgtacacattcccaaggagaga 300
D 3870 TATATATTTATATATTTTACATCCAGGTATCCAGTACATCTGTACATTTCCAGGAGAGA 3811
QY 301 catggtgtcttccaaagcgagacagaagaaggttaaggcagagagagagcagcagtg 360
D 3810 CATGGGTGCTTCCAGGCGAGACAGAAAGGTTAGGCAAGGAGGAGGAGCGACGAGTGC 3751
QY 361 aggcctgggcttgctcacagaagaagctgcagagagcttcagagctgttaagaaggcccgagg 420
D 3750 AGGCTGGGCTTGCTCACAGAAAGTGCAGAGCTTCAGGACTGTAAAGAGGCGCCGGG 3691
QY 421 ctccgagacgcagcaggtact-gagncaaagcagctcctcagctccacagcccgctgcg 479
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QY 480 atccacgccttccgcgaacttcacatcatcatcagagggccgctcatgtcatgacgtt 539
D 3630 ATCCACCGGCTTCTCCGCAAACTTCATCATCATCAGGCGCCGCTCATGTCCAGT 3571
QY 540 gtgcagcgtgc 550
D 3570 GTCCAGCGTGC 3560

RESULT 6
AAH99684
ID AAH99684 standard; cDNA; 1002 BP.
AC AAH99684;
XX
XX 16-OCT-2001 (first entry)
DE Human protein encoding cDNA sequence SEQ ID NO:519.
XX
KW Human; cancer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiallergic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;
KW antiagregant; haemostatic; vulnery; antilucer; osteopathic; eczema;
KW dermatological; antiallergic; antistimatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antineoplastic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopoenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
XX 26-JUL-2001.
PD
XX
PF 22-DEC-2000; 2000MO-US35017.
XX

PR 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX
PA (HYSE-) HYSO INC.
XX
PI Tang YT, Liu C, Dmanac RT;
DR MPI; 2001-457603/49.
DR P-PSDB; AAM25743.
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX
PS Claim 1; Page 577; 1217p; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antinaemic; antiagregant; haemostatic; vulnery;
CC antilucer; osteopathic; dermatological; antiallergic; antistimatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopoenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 1002 BP; 222 A; 259 C; 288 G; 233 T; 0 other;

Query Match 95.2%; Score 528.4; DB 22; Length 1002;
Best Local Similarity 98.5%; Pred. No. 2,9e-132;
Matches 543; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 ttttttttcttaataaacaatttgacaagaaggtgaagaatcctaacaagagtgtg 60
D 40 ttttttttcttaataaacaatttgacaagaaggtgaagaatcctaacaagagtgtg 99
QY 61 aggcacagtgccagcgtgcacgtcagtcacagacagtcgtccacagacgttcacagtggaact 120
D 100 aggcacagtgccagcgtgcacgtcagtcacacaaactcctcagcagcgttcagtggaact 159
QY 121 ggaatggtatataataacagaagaagaagagagactgagtcagagagagagagagagtg 180
D 160 ggaatggtatataataacagaagaagaagagagactgagtcagagagagagagagagtg 219
QY 181 tgaacggagcaacagcactcctagctcttcacattatataatgatatgatatgttccata 240
D 220 tgaacggagcaacagcactcctagctcttcacattatataatgatatgatatgttccata 279
QY 241 tatataattatataattatcatccaggtatccagtcacatctgtacacattcccaaggagaga 300
D 280 tatataattatataattatcatccaggtatccagtcacatctgtacacattcccaaggagaga 339
QY 301 catggtgtcttccaaagcgagacagaagaaggttaaggcagagagagcagcagtg 360
D 340 catggtgtcttccaaagcgagacagaagaaggttaaggcagagagagcagcagtg 399
QY 361 aggcctgggcttgctcacagaagaagctgcagagagcttcagcagctgttaagaaggcccgagg 420
D 400 aggcctgggcttgctcacagaagaagctgcagagagcttcagcagctgttaagaaggcccgagg 459

Query Match 11.4%; Score 63; DB 22; Length 5241;
Best Local Similarity 65.2%; Pred. No. 1.1e-06;
Matches 107; Conservative 0; Mismatches 56; Indels 1; Gaps 1

OY 384 gctgcagaggcgttcacgactgtaagaagggcccggtctgcgcagacgccagtactgag 443
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5233 GCGTGCAGAAATTTTCACAAATACACTGAGGGAGCTGTACTGGCAAAAGCAAATACTGAG 5174

OY 444 -tcaaaagcacgattccatccacgcccgcgtcgatccacgcgcctctccgaacct 502
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5173 CACAAGAACCAGTCCCTCAGAGCTGATTCCACTTCCCTGTGCCAAGGACCTTCTCAGCAAACT 5114

OY 503 tcatcatcatcaggccgcgtcatcgtatcgatccagttgtgcagc 546
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5113 TGATCATGTAGCAGTGCTTCCCTGATGATCTTAGCACAGATTGTGAGC 5070

RESULT 9
AAH10423 standard; cDNA: 557 BP.
AAH10423 ID
AAH10423 standard; cDNA: 557 BP.

AAH10423:
XX AC
XX AAH10423:
XX XX
XX DT 26-JUN-2001 (first entry)
XX DE Human CDNA clone (3'-primer) SEQ ID NO:7258.
XX DE Human CDNA clone (3'-primer) SEQ ID NO:7258.
XX KM Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.
XX KW Homo sapiens.
OS Homo sapiens.
PN EP1074617-A2.
PD EP1074617-A2.
XX PD 07-FEB-2001.
XX XX 28-JUL-2000; 2000EP-0116126.
PE PR 29-JUL-1999; 99JP-0248036.
PR PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX PR
PA (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX PI
DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX PT
XX PS Claim 3; SEQ ID 7258; 2537bp + CD ROM; English.

CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by

	CC	the full-length cDNAs. The primers allow obtaining of the full-length
	CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
	CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
	CC	AAB98893 represent human amino acid sequences; and AAH13629 to AAH13632
	CC	represent oligonucleotides, all of which are used in the exemplification
	CC	of the present invention.
	XX	
SQ	Sequence	357 BP; 111 A; 128 C; 125 G; 185 T; 8 other;
	Query Match	7.8%; Score 43.2; DB 22; Length 557;
	Best Local Similarity	57.4%; Pred.No.0.084; Mismatches 58; Indels 0; Gaps 0;
	Matches 78; Conservative	0; Mismatches 58; Indels 0; Gaps 0;
OY	160	atgcacagagagagacgagtgtcgacggcacacagatcccttagcttcattcatatttat 219
Db	255	atgaggcgaatactaacaggcgttgagccacctgcacctggtcttattttttaacttgcac 314
OY	220	atggatatgatattttctatatatatattattattatttacaccaggtatcccagtcatt 279
Db	315	acgcatattcttctttctcgtatagaagcaactaatatttccctccatgatctcgtgtttt 374
OY	280	cgtaccatttccagcag 295
Db	375	gtctcttcattccaag 390
	RESULT# 10	
	AAH17538/c	
ID	AAH17538 standard; cDNA; 2763 BP.	
XX		
AC	AAH17538;	
XX		
DT	26-JUN-2001 (first entry)	
XX		
DE	Human cDNA sequence SEQ ID NO:17015.	
XX		
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	EPI074617-A2.	
PD		
XX	07-FEB-2001.	
PF	28-JUL-2000; 2000EP-0116126.	
XX		
PR	29-JUL-1999; 99JP-0248036.	
PR	27-AUG-1999; 99JP-0300253.	
PR	11-JAN-2000; 2000JP-0118776.	
PR	02-MAY-2000; 2000JP-0183767.	
PR	09-JUN-2000; 2000JP-0241899.	
PA	(HELI-) HELIX RES INST.	
XX		
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;	
PI	Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;	
XX		
DR	WPI; 2001-318749/34.	
PT		
PR	Primer sets for synthesizing polynucleotides, particularly the 5602	
PT	full-length cDNAs defined in the specification, and for the detection	
PT	and/or diagnosis of the abnormality of the proteins encoded by the	
PT	full-length cDNAs -	
XX		
PS	Claim 8; SEQ ID 17015; 2537pp + CD ROM; English.	
XX		
XX	The present invention describes primer sets for synthesizing 5602	
CC	full-length cDNAs defined in the specification. Where a primer set	
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary	
CC	to the complementary strand of a polynucleotide which comprises one of	
CC	the 5602 nucleotide sequences defined in the specification, where the	
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination	

PR	14-AUG-2000	2000US-0225267
PR	14-AUG-2000	2000US-0225268
PR	14-AUG-2000	2000US-0225270
PR	14-AUG-2000	2000US-0225447
PR	14-AUG-2000	2000US-0225477
PR	14-AUG-2000	2000US-0225757
PR	14-AUG-2000	2000US-0225758
PR	14-AUG-2000	2000US-0225759
PR	14-AUG-2000	2000US-0226279
PR	22-AUG-2000	2000US-0226681
PR	22-AUG-2000	2000US-0226686
PR	22-AUG-2000	2000US-0227182
PR	30-AUG-2000	2000US-0227204
PR	30-AUG-2000	2000US-0228294
PR	01-SEP-2000	2000US-0229287
PR	01-SEP-2000	2000US-0229343
PR	01-SEP-2000	2000US-0229344
PR	01-SEP-2000	2000US-0229345
PR	05-SEP-2000	2000US-0229349
PR	05-SEP-2000	2000US-0229350
PR	05-SEP-2000	2000US-0229513
PR	06-SEP-2000	2000US-0230437
PR	06-SEP-2000	2000US-0230473
PR	08-SEP-2000	2000US-0231242
PR	08-SEP-2000	2000US-0231243
PR	08-SEP-2000	2000US-0231244
PR	08-SEP-2000	2000US-0231414
PR	08-SEP-2000	2000US-0231413
PR	08-SEP-2000	2000US-0232060
PR	08-SEP-2000	2000US-0232061
PR	12-SEP-2000	2000US-0231968
PR	12-SEP-2000	2000US-0232337
PR	14-SEP-2000	2000US-0232338
PR	14-SEP-2000	2000US-0232339
PR	14-SEP-2000	2000US-0232400
PR	14-SEP-2000	2000US-0232401
PR	14-SEP-2000	2000US-0233063
PR	14-SEP-2000	2000US-0233065
PR	14-SEP-2000	2000US-0233065
PR	21-SEP-2000	2000US-0234223
PR	21-SEP-2000	2000US-0234274
PR	25-SEP-2000	2000US-0234997
PR	25-SEP-2000	2000US-0234998
PR	25-SEP-2000	2000US-0234998
PR	25-SEP-2000	2000US-0235484
PR	27-SEP-2000	2000US-0235834
PR	27-SEP-2000	2000US-0235836
PR	29-SEP-2000	2000US-0236337
PR	29-SEP-2000	2000US-0236367
PR	29-SEP-2000	2000US-0236368
PR	29-SEP-2000	2000US-0236369
PR	29-SEP-2000	2000US-0236370
PR	02-OCT-2000	2000US-0236802
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	13-OCT-2000	2000US-0239935
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241121
PR	20-OCT-2000	2000US-0241181
PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	01-NOV-2000	2000US-0244617
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0246675
PR	08-NOV-2000	2000US-0246676
PR	08-NOV-2000	2000US-0246677
PR	08-NOV-2000	2000US-0246678
PR	08-NOV-2000	2000US-0246678
PR	08-NOV-2000	2000US-0246524
PR	08-NOV-2000	2000US-0246525

08-NOV-2000: 2000US-0246526
08-NOV-2000: 2000US-0246527
08-NOV-2000: 2000US-0246528
08-NOV-2000: 2000US-0246532
08-NOV-2000: 2000US-0246609
08-NOV-2000: 2000US-0246610
08-NOV-2000: 2000US-0246611
08-NOV-2000: 2000US-0246613
17-NOV-2000: 2000US-0249207
17-NOV-2000: 2000US-0249208
17-NOV-2000: 2000US-0249209
17-NOV-2000: 2000US-0249210
17-NOV-2000: 2000US-0249211
17-NOV-2000: 2000US-0249212
17-NOV-2000: 2000US-0249213
17-NOV-2000: 2000US-0249214
17-NOV-2000: 2000US-0249215
17-NOV-2000: 2000US-0249216
17-NOV-2000: 2000US-0249217
17-NOV-2000: 2000US-0249218
17-NOV-2000: 2000US-0249244
17-NOV-2000: 2000US-0249245
17-NOV-2000: 2000US-0249264
17-NOV-2000: 2000US-0249265
17-NOV-2000: 2000US-0249297
17-NOV-2000: 2000US-0249299
17-NOV-2000: 2000US-0249300
17-DEC-2000: 2000US-0250160
01-DEC-2000: 2000US-0250391
05-DEC-2000: 2000US-0251030
05-DEC-2000: 2000US-0251038
05-DEC-2000: 2000US-0256719
06-DEC-2000: 2000US-0251479
08-DEC-2000: 2000US-0251856
08-DEC-2000: 2000US-0251868
08-DEC-2000: 2000US-0251869
08-DEC-2000: 2000US-0251989
08-DEC-2000: 2000US-0251990
11-DEC-2000: 2000US-0254097
05-JAN-2001: 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI: 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -

Disclosure: SEQ ID NO 25542; 3071bp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/hematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.

Sequence 2914 BP: 811 A; 676 C; 724 G; 703 T; 0 other;

Query Match 7.1%; Score 39.6; DB 22; Length 2914;
Best Local Similarity 61.8%; Pred. No. 1.6;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Db 210 atattatattggtatgtatttcctatatatatattatattatattacacagta 269
||| ||||| ||| ||| ||||| ||||| ||||| ||| |||
409 atattatatttaaatatattatagttatatatatatatatttttttatatgta 468

Qy 270 tccagtcattcgtaccattccacggagacatgggtcct 311
|| |||| |||| ||||| ||| |||
Db 469 ggttaattcaggttaactccctcctgtggagaagtggaagct 510

RESULT 14
ABL34155
ID ABL34155 standard; DNA; 15548 BP.
XX ABL34155;
XX AC
XX DT 26-MAR-2002 (first entry)
XX DE Human immune system associated gene SEQ ID NO: 2128.
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antihaemic; cytosatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX OS Homo sapiens.
XX PD WO200200928-A2.
XX PN 03-JAN-2002.
XX PD 02-JUL-2001; 2001WO-EP07537.
XX PF 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Pfenbrock C, Berlin K;
XX DR WPI: 2002-130909/17.
XX PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation
XX
PS Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/intestinal bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 other;

Query Match 7.0%; Score 39; DB 24; Length 15548;
Best Local Similarity 71.8%; Pred. No. 5.1;
Matches 51; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db	14094	ttggtttaaataatgcgaagtgtttaacatatgatcttggtttataatacgtatacatagtttta	14153
		}	
Qy	260	cacocaggtaat	270
Db	14154	tatatatatat	14164

RESULT	15
AAQ03743	
ID	AAQ03743 standard; DNA; 2888 BP

Db 1911 ca 1912

Search completed: June 9, 2002, 19:43:45
Job time: 15669 sec

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2002, 12:38:01 ; Search time 7086.26 Seconds

(without alignments)
1638.979 Million cell updates/sec

Title: US-09-853-544-1

Perfect score: 555
Sequence: 1 ttttttttcttaataac.....agttgtgcagcgtgcacaca 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query *
No. Score Match Length DB ID Description

C	1	531.6	95.8	4169	6	AX250159	Sequence
C	2	531.6	95.8	144327	2	AC068353	AC068353 Homo sapi
C	3	531.6	95.8	158104	2	AF284563	AF284563 Homo sapi
C	4	518.6	93.4	604	9	HW073504	AF075060 Homo sapi
C	5	514.2	92.6	63449	2	AC026976	AC026976 Homo sapi
C	6	337.4	60.8	174281	2	AC068338	AC068338 Homo sapi
C	7	265.2	47.8	415	11	G29628	G29628 human STS S
C	8	101	18.2	101	11	G32791	G32791 A009Q42 Hum
C	9	65.8	11.9	80892	2	AC094509	AC094509 Rattus no
C	10	63	11.4	2543	9	AK024793	AK024793 Homo sapi
C	11	63	11.4	5241	6	AX250160	AX250160 Sequence
C	12	63	11.4	131197	2	AC107883	AC107883 Homo sapi
C	13	63	11.4	161492	2	AC016693	AC016693 Homo sapi
C	14	63	11.4	164871	2	AC087465	AC087465 Homo sapi
C	15	45	8.1	189335	2	AC087477	AC087477 Homo sapi
C	16	43.8	7.9	190065	2	AC094728	AC094728 Rattus no
C	17	43.6	7.9	84686	9	AL138685	AL138685 Human DNA
C	18	43.6	7.9	183037	2	AL1390036	AL1390036 Human DNA
C	19	43.4	7.8	189281	2	AL138763	AL138763 Human DNA
C	20	43.4	7.8	2763	9	AK022387	AK022387 Homo sapi
C	21	43.2	7.8	32969	9	AY030284	AY030284 Homo sapi
C	22	43.2	7.8	170071	2	AC084733	AC084733 Homo sapi
C	23	43.2	7.8	183175	2	AC103564	AC103564 Homo sapi
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C	25	42.6	7.7	37393	9	HS023262	Z74619 Human DNA S
C	26	42.6	7.7	142515	9	AC008556	AC008556 Homo sapi
C	27	42.6	7.7	160656	9	AC024258	AC024258 Homo sapi
C	28	42.6	7.7	172039	2	AL356741	AL356741 Human DNA
C	29	42.6	7.7	172264	2	AC099503	AC099503 Homo sapi
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C	33	42.4	7.6	15362	2	AC022244	AC022244 Homo sapi
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C	35	42.4	7.6	256172	2	AC005139	AC005139 Plasmodiu
C	36	42.4	7.6	310779	2	AC005140	AC005140 Plasmodiu
C	37	42.4	7.6	349980	6	AX344569	AX344569 Sequence
C	38	42.2	7.6	89881	9	AL160264	AL160264 Human DNA
C	39	42.2	7.6	111547	2	AP002332	AP002332 Homo sapi
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ALIGNMENTS

RESULT	1	AX250159	4169 bp	DNA	linear	PAT 28-SEP-2001
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DEFINITION	Sequence 4 from Patent WO0166594.					
ACCESSION	AX250159					
VERSION	AX250159.1	GI:15864534				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	1 (bases 1 to 4169)					
JOURNAL	Plozman,G.D., Whyte,D., Manning,G., Sudarsanam,S. and Martinez,R.					
FEATURES	Human protein kinases and protein kinase-like enzymes					
Source	Patent: WO 0166594-A 4 13-SEP-2001;					
	Sugen, Inc. (US)					
	Location/Qualifiers					
	1..4169					
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BASE COUNT 871 a 1398 c 1167 g 733 t
ORIGIN

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Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 121 ggaatgtgtataatcagaagaacacagggagagacttagtcagagagagagagatg 180
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DB 3990 GGAATGTGTATATATACAGAAACAGGAGAGACTTAGTCAGAGAGAGAGAGAGTG 3931

QY 181 tgaagcggcaacagcactccttagtcttcattatattatataatgtatattcattata 240
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QY 241 tatataattatataattacatccaggtatccagtcactgttaccattcccccagagaga 300
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DB 3870 TATATATATATATATTTTAAATCCAGATATCCAGTATCTGTACATTTCCACAGGAGA 3811

QY 301 catgggtgtcttccaaggcgaagaaagggttaaggcagggagggcgacaggtgtc 360
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DB 3810 CATGGGTGCTTCCAAAGCGAGACAGAAAGGTTAGGACGAAAGGGGCGACGACGTGC 3751

QY 361 agcgtgggggtgtgtacagaagctgtcagagcttgcagagctgttaaggagggccggg 420
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DB 3750 AGCGTGGGGCTTGGCTACAGAGAGCTGCAGAGAGCTTACGACGTATAGAGGGCCCGGG 3691

QY 421 ctcgcagacgcaggtact-gagncacaaagccagtcctcagctccacgcccgcctgcg 479
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DB 3690 CTCGCGAGACGCCAGGTACTGGGACAGCAACCCAGTCTCTCCAGTCCACGCCGCCGCTGCG 3631

QY 480 atccacgccttctcgcgaactcatcatcatcagggccgcgttcattgcagtcagtt 539
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QY 540 gtgcagcgtgc 550
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DB 3570 GTGCAGCGTGC 3560

RESULT 2
LOCUS AC068353 144327 bp DNA linear HTG 13-FEB-2002
DEFINITION Homo sapiens chromosome 8 clone RP11-399J23 map 8, ** SEQUENCING
ACCESSION AC068353
VERSION AC068353.11 GI:18653561
KEYWORDS HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVERFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144327)
REFERENCE 1 (bases 1 to 144327)
TITLE Homo sapiens chromosome 8, clone RP11-399J23
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 144327)
    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
    Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
    Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,
    Campolongo,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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    Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L.,
    Grand-Pierre,N., Grant,G., Hages,B., Heathford,A., Horton,L.,
    Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
    Klein,D., Lakocque,K., Lamazares,R., Landers,T., Lehoczek,J.,
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    O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
    Pisanl,C., Pollara,V., Raymond,S., Severy,P., Spencer,B.,
    Roy,A., Santos,R., Schauer,S., Stojanovic,N., Subramanian,A., Talamas,J.,
    Stange-Thomann,N., Stojanovic,N., Travers,M., Trigglio,J.,
    Testafte,S., Theodore,J., Tirrell,A., Travers,M., Trigglio,J.,
    Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
    Young,G., Zainoun,J., Zimmer,A. and Zody,M.
    Direct Submission
    Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome
    Research, 320 Charles Street, Cambridge, MA 02141, USA
    On Feb 13, 2002 this sequence version replaced g1:18583956.
    All repeats were identified using RepeatMasker:
    Smit, A.F.A. & Green, P. (1996-1997)
    http://ftp.genome.washington.edu/RM/RepeatMasker.html
    ----- Genome Center
    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: MIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence_submissions@genome.wi.mit.edu
    ----- Project Information
    Center project name: L10145
    Center clone name: 399_J_23
    * NOTE: This is a 'working draft' sequence. It currently
    * consists of 3 contigs. The true order of the pieces
    * is not known and their order in this sequence record is
    * arbitrary. Gaps between the contigs are represented as
    * runs of N, but the exact sizes of the gaps are unknown.
    * This record will be updated with the finished sequence
    * as soon as it is available and the accession number will
    * be preserved.
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    Matches 545; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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    DB 56128 GGAATGTGTATATATACAGAAACAGGAGAGACTTAGTCAGAGAGAGAGAGAGTG 56187

    QY 181 tgaagcggcaacagcactccttagtcttcattatattatataatgtatattcattata 240
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    DB 56188 TGGACGGGCAACAGCATCTTAGCTTCAATATTATATGATATGATATTTCATATA 56247

    QY 241 tatataattatataattacatccaggtatccagtcactgttaccattcccccagagaga 300

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Qy	480	atccacgcgcctcttcgcgaactcatcatcatcagggccgcgctcatalgctgcatcagtt	539
Db	66476	ATCCACGCCCTTCTCCGCAAACTTCATCATCATTCAGGGCGCGCTTCATGTCATCCAGTT	66417
Qy	540	gtgcagcgtgc 550	
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RESULT	4			PRI 04-AUG-1998
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LOCUS	HOMO sapiens	604 bp	mRNA	linear
DEFINITION	Homo sapiens full length insert cDNA y073E04.			
ACCESSION	AJ075060			
VERSION	AF075060.1	GI:3377601		
KEYWORDS	FLI-CDNA,			
SOURCE	human.			

REFERENCE
AUTHORS

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 604)
Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J.,

TITLE
Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Unpublished 2 (bases 1 to 604) Waterston, R. Direct Submission Submitted (30-JUN-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	SUBMITTED BY: Genome Sequencing Center Department of Genetics Washington University St. Louis MO 63108 USA http://genome.wustl.edu/gsc mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.

FEATURES
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Matches 532;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1

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OY	134	attacagaagaanaacagagagagactagtgacagagagagagacagatgtgtgaagggacaca	193
Db	484	ATTACAGAAGAANAACAGGAGGAGACTTAGTGCACAGAGGAGAGACAGTGTGACGGCGACA	425
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OY	374	gtccacagaaagctgcagagagcttcacagactgtlaagagggcccccggctcgcagaaagcc	433
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ACCESSION	AC026976		SEQUENCE SAMPLING.
VERSION	AC026976.2	GI:13443237	
KEYWORDS	HTG; HTGS_PHASEO.		
SOURCE	human.		

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	2 (bases 1 to 63449)
Barren, B., Linton, L., Nusbaum, C. and Lander, E.	Unpublished
Homo sapiens, clone RP11-792016	2 (bases 1 to 63449)
Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,	

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beeda, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Bugnion, M., Calkins, D., Campbell, R., Chang, Y., Chaudhry, H., Chavakis, T., Chhabra, A., Coleman, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collamore, A., Domlo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Dodge, S., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Garrett, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, E., Han, J., Harbeck, B., Hendricks, M., Howell, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A., Klein, J., LeRoque, K., Lamazeres, R., Landers, T., Lehoczyk, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCafferty, M., McEwan, P., McGuck, A., McKenna, C., McPheeates, R., Melcham, J., Meunus, L., Mihov, T., Miranda, C., Mlenka, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivar, F.M., Oliver, J., Peterson, K., Pierre, N., Plisack, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.

TITLE
JOURNAL

COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 24, 2001 this sequence version replaced g1:7328855.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 18651
Center clone name: 792_O_16

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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* 56073 56172: gap of 100 bp

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Query Match 92.6%; Score 514.2; DB 2; Length 63449;
 Best Local Similarity 98.0%; Pred. No. 1e-125;
 Matches 541; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

```

QY 1 ttttttttcttaataacaatttgcacaaagggtggaagaatccttaacaaagctatg 60
    |||
DB 49030 TTTTTCCTTTAAATTAACAATTTCACAAAAGGTAAGAAATTCCTAAACAAGATTG 49089
    |||
QY 61 aggcagctctccagctgcatcttcacacagactgctccagacgttgcagtaact 120
    |||
DB 49090 AGCCCACTGCCAGCTGCATTCAGTTCCACAGACTGCTCTCAGACGTTGCTTGAAC 49149
    |||
QY 121 ggaatctgtataataacagaagaacagggaggaactagtcagagagagagagagatg 180
    |||
DB 49150 GGAATGCTATTAATTAACAGAAAGAAACAGAGGAGCTTATTCACAGAGAGAGAGAG 49209
    |||
QY 181 tgaagagggaagagacactgcttgcttcatattatataatgatatatattttata 240
    |||
DB 49210 TGACCGGCAACAGCAATCCTTACTTTCATATTATTAATGATATGATATTCTTATA 49269
    |||
QY 241 tatatatatatattatcatcaccaggtatccagtcacatctgtaccattccacaggaga 300
    |||
DB 49270 TATATATTATATATTATTACATCCAGTATCCAGTCACTCTGACATTTCCAGGGAGA 49329
    |||
QY 301 catggctgtctccaagcgagacaggaagaggttaaggcagggagagcgacggtgc 360
    |||
DB 49330 CATGGCTGCTCCAGACGACAGAGAAAGGGTTAGGACAGGAGGACGACGCTGC 49389
    |||
QY 361 agctgtggcttggctcacaagaagctgctgaggtcttcaacagct-gtaagagggcccg 419
    |||
DB 49390 AGCTGTGGCTTGCTCCACAGAACTGACAGACTTTCACGATGGGAAAGAGGCCCGG 49449
    |||
QY 420 gctccgcaagcgcaaggtact-gagncaaagcagctccctcagctcacgcccccgctgc 478
    |||
DB 49450 GCTCCCTCAACGCGCAAGTACTGCGACAAAGCAGTCTCCAGCTCCAGCCCCGCTGC 49509
    |||
QY 479 gatccaacgctcttcgcgaacattcatcatcagggcccgctcatctgcatcag 538
    |||
DB 49510 GATCCACGCCCTTCTCCGAAACTTCATCATCATCAGGCGCGCTTCATGTCATCAGT 49569
    |||
QY 539 tctgcagcgctgc 550
    |||
DB 49570 TCTGCAGCGCTGC 49581
    |||

```

RESULT 6
 AC068338 AC068338 174281 bp DNA linear HTG 01-DEC-2001
 LOCUS

DEFINITION Homo sapiens chromosome 11 clone RP11-817013 map 11, WORKING DRAFT
 SEQUENCE, 12 unordered pieces.
 AC068338
 AC068338.5 GI:17223174
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 174281)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 11, clone RP11-817013
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 174281)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bede, F.,
 Boguslavsky, L., Bouknight, B., Brown, A., Burkett, G.,
 Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collamore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Glende, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hags, B., Heatford, A., Horton, L.,
 Howard, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A.,
 Klein, J., Lacombe, K., Lamazares, R., Landers, T., Lehotzky, J.,
 Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
 McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R.,
 Melrim, J., Menus, L., Mihova, T., Miranda, C., Mlewa, Y., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Tassell, S., Theodore, J., Tjrell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT
 Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Dec 1, 2001 this sequence version replaced gi:15290773.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L10087
 Center clone name: 817_O_13

----- Summary Statistics
 Sequencing vector: M13; M77815; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 167722 bases at least Q40
 Consensus quality: 169015 bases at least Q30
 Consensus quality: 170603 bases at least Q20
 Insert size: 177000; agarose-fp
 Insert size: 173181; sum-of-contigs

Quality coverage: 12.6 in Q20 bases; agarose-fp
 Quality coverage: 12.9 in Q2.
 NOTE: This is a 'working draft' sequence. It currently
 consists of 12 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 107104: contig of 107104 bp in length
 * 107105 107204: gap of 100 bp
 * 107205 107765: contig of 561 bp in length

```
* 107766 107865: gap of 100 bp
* 107866 108310: contig of 445 bp in length
* 108311 108410: gap of 100 bp
* 108411 109129: contig of 719 bp in length
* 109130 109229: gap of 100 bp
* 109230 109871: contig of 642 bp in length
* 109872 109971: gap of 100 bp
* 109972 110628: contig of 657 bp in length
* 110629 110728: gap of 100 bp
* 110729 112287: contig of 1559 bp in length
* 112288 112387: gap of 100 bp
* 112388 113548: contig of 1161 bp in length
* 113549 113648: gap of 100 bp
* 113649 113950: contig of 2302 bp in length
* 113951 116050: gap of 100 bp
* 116051 119604: contig of 3554 bp in length
* 119605 119704: gap of 100 bp
* 119705 135629: contig of 15925 bp in length
* 135630 135728: gap of 100 bp
* 135730 174281: contig of 38552 bp in length.
```

FEATURES

```
source
1. 174281
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-817013"
/clone_lib="RPC1-11 Human Male BAC"
1. 107104
/note="assembly-fragment
clone_end:SP6
vector_side:left"
misc_feature
107205..107765
/note="assembly-fragment"
misc_feature
107866..108310
/note="assembly-fragment"
misc_feature
108411..109129
/note="assembly-fragment"
misc_feature
109230..109871
/note="assembly-fragment"
misc_feature
109972..110628
/note="assembly-fragment"
misc_feature
110729..112287
/note="assembly-fragment"
misc_feature
112388..113548
/note="assembly-fragment"
misc_feature
113649..115950
/note="assembly-fragment"
misc_feature
116051..119604
/note="assembly-fragment"
misc_feature
119705..135629
/note="assembly-fragment"
misc_feature
135730..174281
/note="assembly-fragment
clone_end:T7
vector_side:right"
ORIGIN
BASE COUNT 42539 a 44506 c 43805 g 42321 t 1110 others
```

Query Match 60.8%; Score 337.4; DB 2; Length 174281;
Best Local Similarity 90.8%; Pred. No. 1.5e-78;
Matches 435; Conservative 0; Mismatches 35; Indels 9; Gaps 7;

```
OY 77 tgcattcagttcacagaactgtccctccagacgttgatgtaagaatgtgtataatt 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107212 TGCATTTCAGTCAACAGACTGTCGCCAGACGTTGCATGCACTGGAATGTATTA-T 107270

OY 137 acagaagaagaacagagagactagtcacagagagagacagtgctgacgagcaacagca 196
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107271 ACAGAAGAAGAAGAGGAGAGCTTAGTGACAGAGAGAGAGAGAGTGTGACGGCAACAGCA 107330

OY 197 tccctagcttcattcatattatataatgtgtatatttctctatatataattatata-- 254
```

```
||||| ||||||| ||||||| ||| | | | | |
DB 107331 TCCTTAGTCTTCA-ATTTATATATGATATGATTTTGAAGTGAAGACTTCANTNTA 107389

OY 255 -ttcacacacaggtatccacagtcacgtctacaca-tttccagagagacatggtcttc 312
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107390 GTTTTACATCCAGGATCCAGTCACTATCTTACCACTTTTCCAGGAGACATGGGCTTTC 107449

OY 313 caagcgagacaggaagaggttagcagaggaagggcagcagctgcagctgagggctt 372
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107450 CAAGCGAGACAGAGAAAGGTTATAGCGAGGAGGAGGAGGAGCGTGCAGGCTGGGGCTT 107509

OY 373 ggcctcacaaagctgcaggaagcttgcagcagctgttaagaagagcccggtcttcgcaagc 432
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107510 GGCCTC-CAGAGAGCTGCAGGAGCTTC-GCAGCTGTATAGAGGGCCCGGCTCCGCAAGCGC 107567

OY 433 caggtact-gagucaaagccagctccctcagctccaccccgctcgtacacagcctt 491
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107568 CAGGTACTGCGACAAAGCCAGTCTCTCCAGCTTCACAGCCCGCTCTGCATCCAGCCCTT 107627

OY 492 ctccgcaacttcatacatcagcagcccgctcatgtcgatccagttgtgcagcgtgc 550
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 107628 CTCGCAAACTCTTCTCTNTGTCAGGCGCCGCGCATGTCGATCCAGTTGTGACGCGTGC 107686
```

RESULT 7

G29628 415 bp DNA linear STS 05-OCT-1996
LOCUS human STS SHGC-34242, sequence tagged site.
DEFINITION G29628
ACCESSION G29628
VERSION G29628.1 GI:1593179
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
REFERENCE
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, W-344, Stanford, CA 94305, USA
Tel: 415/725/9687
Fax: 415/725/9689
Email: myers@shgc.stanford.edu

Primer A: TTGACAAAGGTCGAGAA
Primer B: TCGTCTGCACTAGTCCTC
STS size: 150
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from H44044
-- Washington University/Merck EST sequence.

FEATURES
source 1. .415 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="8"
STS
primer_bind 1. .150
primer_bind 1. .21
complement(129. .150)
BASE COUNT 106 a 84 c 120 g 95 t 10 others
ORIGIN

Query Match 47.8%; Score 265.2; DB 11; Length 415;
Best Local Similarity 86.7%; Pred. No. 6.7e-60;
Matches 357; Conservative 0; Mismatches 43; Indels 12; Gaps 6;

23 ttgacaaaagggtgagaatccctaaacaggtattgaagcagctgcagctcatt 82
|||||
1 TTTGACAAAAGGCTGAGAAATCTTAAACAGGTATTGAGCCAGTGTCCAGCTGCATT 60
|||||
83 cagttcacagaactgtctcagagcgttcagtgaaactggaaatgttataacagaa 142
|||||
61 CAGTTCACAGAACTGCTCAGCAGCGTGCATGGAAGTGAATGTATATTATTCAGAA 120
|||||
143 gaaacagagagagacttagtcagagaagagacagctgtgagcggcaacagcattc 202
|||||
121 GAAACAGGAGAGACTTAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
|||||
203 gtcttcattatattatagtgatgatagtatttctatataatataatattacat 262
|||||
181 GTCTTCATATTATATATGATATGATATGATATTCCTATATATATATATATATATAT 240
|||||
263 cca-ggatccacagtcacatcgtacattccca-ggagacacatgggtgcttccaaagcga 320
|||||
241 CCNGGGNNTCGCCAGTCATCTGATTCATTCGCCAGGAGAGAGAGAGAGAGAGAGAG 300
|||||
321 gaaa-aaagaggttagagcagg-aaagggcagcagcagcagcagcagcagcagcagc 372
|||||
301 GAAACAGGAGAGAGGTAGGCGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
|||||
373 -ggctacagaaagctgcagagac-ttcacagcagctgtaagaagggcccgagcct 422
|||||
361 GGCTNACAGAGACTTCAGGGGCTTTCAGACATTTTAAGGGGGCCCGCGT 412
|||||

RESULT 8
G32791 101 bp DNA linear STS 24-SEP-1999
LOCUS G32791
DEFINITION A009042 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G32791
VERSION G32791.1 GI:5923312
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 101)
AUTHORS Adams M.D.
TITLE Human STS sequences
JOURNAL Unpublished
COMMENT Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Email: mdadams@tigr.org
Primer A: ATGCACTGGAATGCTATTAAT
Primer B: ATATCAAGACTAAGATGCTGT
STS size: 101
PCR Profile:
Denaturation: 96C 5min
Anneal: 54C 30sec
Extend: 72C 30sec
Denature: 95C 30sec

FinalExtend: 72C 5min
Cycles: 30
Protocol:
GenomicDNA: 25 ng
primers: 0.43 uM each
dNTPs: 230 uM each
Amplified: 0.5 units
tagstart Ab: 0.5 units
Total Volume: 10 ul
Buffer:
Tris-HCl pH8.8: 100 mM
KCl: 500 mM
MgCl2: 20 mM
Tris-HCl X-100: 1%
Concentration: 10X
Prepared with primer pairs derived from THC129699: GenBank
Accession Numbers: R70141, H4044, L73763.
Location/Qualifiers
1. .101
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human"
STS
primer_bind 1. .101
primer_bind 1. .23
complement(79. .101)
BASE COUNT 35 a 14 c 30 g 22 t
ORIGIN

Query Match 18.2%; Score 101; DB 11; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

113 atggaactggaatggtatattacagaagaagaaggagacttagtcagagaaga 172
|||||
1 ATGGAAGTGAATGATGATTAATTAACAGAGAAACAGGAGAGAGAGAGAGAGAGAGAG 60
|||||

173 gacgaagtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 213
|||||
61 GAGCACTGTGAGAGCGGCAACAGCATCTTAGCTTCATAT 101
|||||

RESULT 9
AC094509 80892 bp DNA linear HTG 20-DEC-2001
LOCUS AC094509/c
DEFINITION Rattus norvegicus clone CH230-4E17, *** SEQUENCING IN PROGRESS ***
ACCESSION AC094509
VERSION AC094509.3 GI:17941241
KEYWORDS HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 80892)
AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Ali-oshman F.R., Allen C.,
Alsbrooks S.L., Amaralunga H.C., Are J.R., Banks T., Barbara J.,
Benton J., Blinze K., Blankenburg K., Bonini D., Bouck J.,
Bowling S., Brieval M., Brown E., Brown M., Bryant N.P., Butay C.,
Burke P., Burke C., Burrell K.L., Byrd N.C., Caron T.F.,
Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R.,
Chen Z., Chowdhry I., Christopoulos C., Cleveland C.D., Cox C.,
Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C.,
Davy Carroll L., Dederich D.A., Delaney K.R., Delgado O.,
Denn A.L., Ding Y., Dinh H.H., Douhaite K.J., Draper H.,
Dugan-Rocha S., Durbin K.J., Earnhart C., Edgar D., Edwards C.C.,
Elhaj C., Escotto M., Falls T., Ferraguto D., Flagg N., Ford J.,
Foster P., Frantz P., Gabisi A., Gao J., Garcia A., Garner T.,
Garza N., Gill R., Gorrell J.H., Guevara M., Gunaratne P., Hale S.,
Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A.,

Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvath, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Lunn, R.,
Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhney, E., McLeod, M. P., Mendor, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Ogulu, M., Okwou, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shoostari, N.,
Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Swatek, A., Taber, P., Tamerisa, A., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellrod, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 80892)
Worley, K. C.

Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15799320.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAUD
Center clone name: CH230-4E17
----- Summary Statistics
Assembly program: Phrap; version 0.990329first call to
findhaplalist
Consensus quality: 56832 bases at least Q40
Consensus quality: 63643 bases at least Q30
Consensus quality: 67630 bases at least Q20
Estimated insert size: 39832; sum-of-contris estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.4x in Q20 bases; sum-of-contris estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
2037 2036: contig of 2036 bp in length
2137 2136: gap of unknown length
5541 5540: contig of 3404 bp in length
5641 5640: gap of unknown length
7154 7154: contig of 1514 bp in length
7254 7254: gap of unknown length
10126 10126: contig of 2872 bp in length
10226 10226: gap of unknown length
12204 12204: contig of 1978 bp in length
12304 12304: gap of unknown length
14032 14032: contig of 1728 bp in length
14033 14032: gap of unknown length

14133 16701: contig of 2569 bp in length
16702 16801: gap of unknown length
16802 16931: contig of 2130 bp in length
16932 19031: gap of unknown length
19032 20670: contig of 1639 bp in length
20671 20770: gap of unknown length
20771 23399: contig of 2629 bp in length
23399 23499: gap of unknown length
23499 25649: contig of 2150 bp in length
25649 25749: gap of unknown length
25750 27707: contig of 1988 bp in length
27708 27807: gap of unknown length
27808 29187: contig of 1380 bp in length
29187 29287: gap of unknown length
29288 30599: contig of 1312 bp in length
30600 30699: gap of unknown length
30700 32012: contig of 1313 bp in length
32012 32112: gap of unknown length
32113 33114: contig of 1002 bp in length
33114 33214: gap of unknown length
33215 34609: contig of 1395 bp in length
34610 34709: gap of unknown length
34710 35952: contig of 1243 bp in length
35953 36052: gap of unknown length
36053 37791: contig of 1739 bp in length
37792 37891: gap of unknown length
37892 39196: contig of 1305 bp in length
39197 39296: gap of unknown length
39297 40805: contig of 1509 bp in length
40806 40905: gap of unknown length
40906 42389: contig of 1464 bp in length
42389 42489: gap of unknown length
42490 43940: contig of 1451 bp in length
43941 44040: gap of unknown length
44041 45314: contig of 1274 bp in length
45315 45414: gap of unknown length
45415 46689: contig of 1275 bp in length
46690 46789: gap of unknown length
46789 48037: contig of 1248 bp in length
48038 48137: gap of unknown length
48138 49753: contig of 1616 bp in length
49754 49853: gap of unknown length
49854 51676: contig of 1823 bp in length
51677 51776: gap of unknown length
51777 52788: contig of 1012 bp in length
52789 52888: gap of unknown length
52889 54070: contig of 1182 bp in length
54071 54170: gap of unknown length
54171 55190: contig of 1020 bp in length
55191 55280: gap of unknown length
55291 55360: contig of 1270 bp in length
55361 56660: gap of unknown length
56661 58150: contig of 1490 bp in length
58151 58250: gap of unknown length
58251 59449: contig of 1199 bp in length
59450 59549: gap of unknown length
59550 61139: contig of 1590 bp in length
61140 62362: contig of 1123 bp in length
62363 62462: gap of unknown length
62463 63610: contig of 1148 bp in length
63611 63710: gap of unknown length
63711 64847: contig of 1137 bp in length
64848 64947: gap of unknown length
64949 66262: contig of 1315 bp in length
66263 66362: gap of unknown length
66363 67452: contig of 1090 bp in length
67453 67552: gap of unknown length
67553 68667: contig of 1315 bp in length
68668 68967: gap of unknown length
68968 70101: contig of 1134 bp in length
70102 71230: gap of unknown length
71230 71230: contig of 1029 bp in length

OY	444	-ncaagacgcatctcccgagccttcacggcccgcgttcgaagccacgccgccttccccaact 502
Db	5173	CACAAAGCCAGTCCTCCAAGGCTGTATTCCACTTCTCCTGTCCAGGAGCACTTTTCAGCAACT 5114
OY	503	tcaatcatacgaaggcccgcttcatactgatccagtctgtgcagc 546
Db	5113	TGATCATGACGACGATGTCTCGCTGTGATGTCTAGCAGCACTTTTGAGGC 5070
RESULT	12	
LOCUS	AC107883/c	
DEFINITION	131197 bp DNA linear HTG 24-JAN-2002	
ACCESSION	AC107883	
VERSION	AC107883.1	
KEYWORDS	Homo sapiens chromosome 15 clone CTD-2318C11 map 15, WORKING DRAFT SEQUENCE, 4 ordered pieces.	
SOURCE	HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 131197) Birten,B., Linton,L., Nusbaum,C. and Landier,E. Homo sapiens chromosome 15, clone CTD-2318C11 unpublished 2 (bases 1 to 131197) Birten,B., Linton,L., Nusbaum,C., Landier,E., Ali,A., Allen,N., Anderson,S., Barina,N., Bastien,V., Boguslavskiy,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.J., Chazarro,B., Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArrellano,K.K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Grinde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamzares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Melidris,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M. Direct Submission Submitted (24-Jan-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html	
JOURNAL COMMENT	Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Web site: http://www.seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Project Information Center project name: 122183 Center clone name: 2318_C_11 Summary Statistics Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 130512 bases at least Q40 Consensus quality: 130627 bases at least Q20 Consensus quality: 130721 bases at least Q20 Insert size: 127000; agarose-fp Insert size: 130897; sum-of-contigs Quality coverage: 16.1 in Q20 bases; agarose-fp	

```

Quality coverage: 15.6 in Q20 bases; sum-of-ctrligs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 ctrligs. Gaps between the ctrligs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 15983: contig of 15983 bp in length
* 15984 16083: gap of 100 bp
* 16084 46826: contig of 30743 bp in length
* 46827 46928: gap of 100 bp
* 46927 90567: contig of 43641 bp in length
* 90568 90667: gap of 100 bp
* 90668 131197: contig of 40530 bp in length.
FEATURES
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/map="15"
/clone="CMD-2318C11"
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/note="assembly_fragment"
46927..90567
/note="assembly_fragment"
90668..131197
/note="assembly_fragment"
misc_feature
BASE COUNT 34710 a 31848 c 31069 g 33269 t 301 others
ORIGIN
Query Match 11.4%; Score 63; DB 2; Length 131197;
Best Local Similarity 65.2%; Pred. No. 1.6e-05;
Matches 107; Conservative 0; Mismatches 56; Indels 1; Gaps 1;
DB 55142 GCTGCGAGATTTCACAATACACTGAGGGAGCTGTGACTGCACAAAGCCAAATCTGAG 55083
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 444 -ncaagccagctcctccagcgtcgaacgcccgcctcgatcacaccgcttcctccgaact 502
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 55082 CACAAAGCCAGTCCCAAGCGCATTCACCTTCCCTGTGCCAGGAGACTTTCTAGCAACT 55023
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 503 lcatcatcatcaggccgctcatgatcagttgltgcagc 546
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 55022 TGATCATGAGCAGTGTCGCTTGATGCTAGCCAGTTTGGAGC 54979
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 13
ACOL16693/c 161492 bp DNA linear HTG 07-JUL-2000
LOCUS ACOL16693/c
DEFINITION Homo sapiens chromosome 15 clone Rp11-9AP14, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
ACCESSION ACOL16693
VERSION ACOL16693.4 GI:7230876
KEYWORDS HTG; PHASE1; HTGS; DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 161492)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 161492)
AUTHORS Waterston,R.H.
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